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THESIS

**MOLECULAR DYNAMIC MODELING AND SIMULATION
FOR POLYMERS**

by

Anthony F. Harrell

September 2003

Thesis Advisor:

Young W. Kwon

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MOLECULAR DYNAMIC MODELING AND SIMULATION FOR POLYMERS

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Submitted in partial fulfillment of the
requirements for the degree of

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from the

**NAVAL POSTGRADUATE SCHOOL
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ABSTRACT

Polymers have been widely used in various engineering applications. For more than a quarter century, the materials have been utilized intensively for the binding materials for composites. The material properties of the binding materials called matrix materials play an important role for the composite material behaviors. As a result, the objective of this study was to understand the mechanical properties of polymers. In particular, the goal was to develop insights as to how a molecular level structure is connected to the bulk properties of materials assuming homogeneity. To this end, molecular dynamics was used to model and simulate the polymeric behaviors. Polymeric chains were modeled using the bead and spring model along with interacting potentials. The study examined the effects of different sizes, densities, and numbers of molecules per chain on the shear moduli of the polymers. Furthermore, some preliminary study was also conducted for metallic particle reinforced polymer composites.

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I. INTRODUCTION

A. MECHANICAL PROPERTIES

Mechanical properties are the totality of components determining the bodies' response to external and mechanical influences. All of this is manifested in the ability for the bodies to develop reversible and irreversible deformations and to resist failure. Determining material performance requires defining a force constant or Young's modulus. One of two key parameters for this determination is stress, the amount of applied force. The second parameter is strain, the displacement. With the use of molecular dynamics simulations, polymer properties as well as behaviors can be investigated on a nano-scale.

B. PURPOSE OF MOLECULAR DYNAMICS

Due to the wide applications in technology for polymer usage, the characteristic behaviors of polymer materials have become of theoretical and experimental interest. The methodology employed includes molecular dynamics simulation that uses models representing the molecules at various levels of detail. The behaviors of molecules close to interfaces, in thin films and in confining geometries, have attracted growing interest from both the theoretical and applications points of view [1].

Shear modulus is one of important properties of which molecular dynamics is used to observe the behavior. Polymer simulation embraces a broad range of factors to pinpoint the behavior. There is a state of constant movement by the polymers in which the presence of solid surfaces strongly influences the matrix properties [2]. A picture of a molecular dynamic model is shown in Figure 1. The goal is to develop new insights as to how a molecular structure, and dynamics, is connected to the bulk properties of materials. The force fields for the polymer chains are clearly seen in Figure 2.

Molecular Dynamics computer simulations are also used to observe the molecular motions between particles and composites. The study of how nanoparticles influence the structure and dynamics of polymers can be done in great detail through the use of

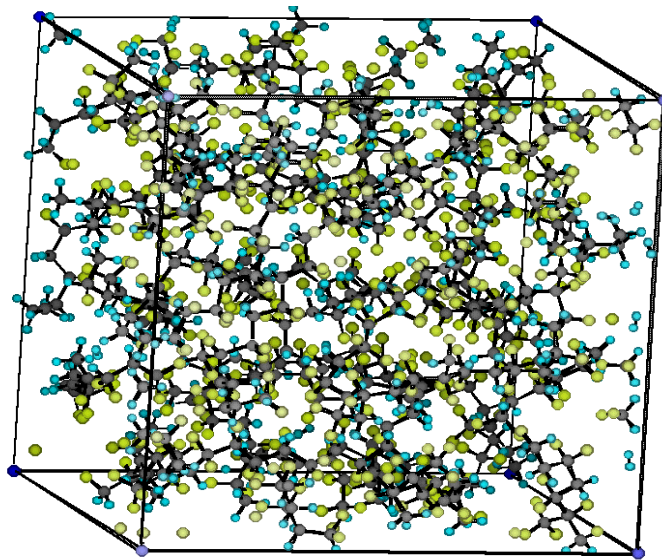


Figure 1. Molecular Dynamic Simulation

molecular simulations. Computer simulation approaches provide a detailed molecular description of polymer chains' behavior that lead to new insights into materials properties.

The Force Field

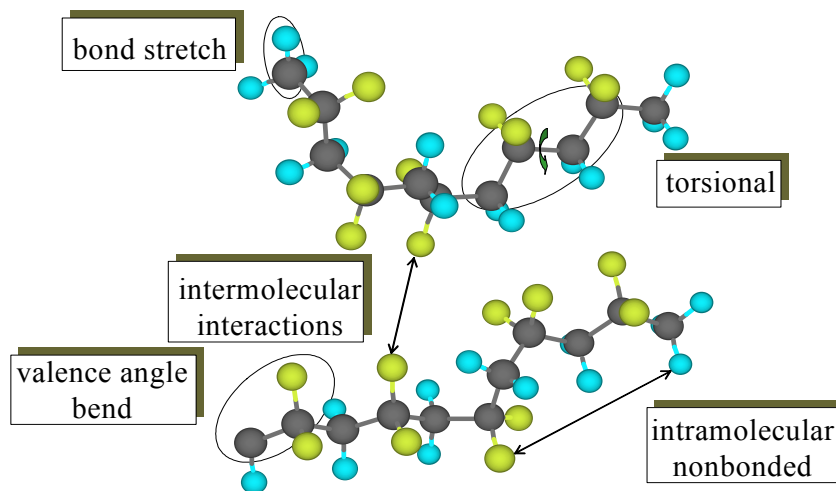


Figure 2. Force Field for MD Simulations

C. BACKGROUND

1. Polymers

Long chain molecules called polymers are the foundation for major products of various industries today. Polymers are used to make a range of different types of products as summarized in the table below. These materials have so many varied characteristics and applications that their usefulness can only be measured by the imagination.

A polymer is a large molecule formed by joining many small ‘monomer’ units. Many common classes of polymers are composed of hydrocarbons. Carbon makes up the backbone of the molecule, and hydrogen atoms are bonded along this backbone.

| Polymer Type | Example of use |
|--------------|------------------------------------|
| Fibers | Nylon |
| Plastics | Films, moldings |
| Elastomers | Rubbers |
| Coatings | Kitchen worktops, food-can linings |
| Others | Biodegradable materials |

Table 1 Polymer Uses

2. Molecular Dynamics

In many cases, molecular dynamics simulations are based on the Lennard-Jones potential of inter-atomic interactions. For a pair of atoms i and j located at r_i and r_j , the potential energy is given by [3]:

$$U_{LJ}(r_{ij}) = 4\zeta \left[\left(\frac{\tau}{r_{ij}} \right)^{12} - \left(\frac{\tau}{r_{ij}} \right)^6 \right],$$

where $\vec{r}_{ij} = \vec{r}_i - \vec{r}_j$, $r = |\vec{r}_{ij}|$, ζ and τ are phenomenological parameters specific to each material system. The Lennard-Jones potential features a short-range repulsive potential,

together with a long-range attractive potential. The $1/r^6$ attractive potential arises from fluctuating dipole moments on neutral atoms, while the $1/r^{12}$ term models the short-range repulsion that arises from the Pauli exclusion effects of overlapping electron clouds. The Lennard-Jones potential defines the repulsion, attraction and finally the cutoff range where the potential no longer is applicable. The first simplification in molecular dynamics is to ignore the attractive tail. This modifies the above equation to:

$$U_{LJ}(r_{ij}) = 4\zeta \left[\left(\frac{\tau}{r_{ij}} \right)^{12} - \left(\frac{\tau}{r_{ij}} \right)^6 \right] + \zeta, \quad r_{ij} \leq r_c = 2^{1/6} \tau,$$

with the cut-off radius, r_c , chosen such that $U(r_c) = 0$. The desired result is for the force of the interaction that is given by $\vec{f} = -\nabla U(r)$ to result in:

$$\vec{f}_{ij} = \frac{48\zeta}{\tau^2} \left[\left(\frac{\tau}{r_{ij}} \right)^{14} - \frac{1}{2} \left(\frac{\tau}{r_{ij}} \right)^8 \right] \vec{r}_{ij}.$$

As r increases to r_c , the force drops to zero, and this prevents any discontinuities.

3. Crosslinking Density

Molecular dynamics simulations are heavily demanded for the study of randomly cross-linked polymers. Barsky and Plischke previously reported on simulations that involved short chains and small system sizes [4]. These simulations “demonstrated the existence of a universal function $P(\xi)$ that describes the distribution of localization lengths for a wide range of crosslink density” [4]. The relationship between the shear modulus and density were never taking into account. During later studies, Barsky and Plischke extended their simulations to longer polymer chains and systems [4]. Their focused was on the shear modulus $E(n)$ as a function of the density of crosslinks n .

The purpose of the crosslinks is to tie all the polymer molecules together. This prevents molecules from flowing past or around each other once the temperature increases, and also increases their resistance to melting. The advantage of being tied together is that they are not easily broken apart from each other. The difference between single uncrosslinked polymer chains and a crosslinked network is described in Figure 3.

However, in this experiment the temperature was held constant as well as the cross-linking density.

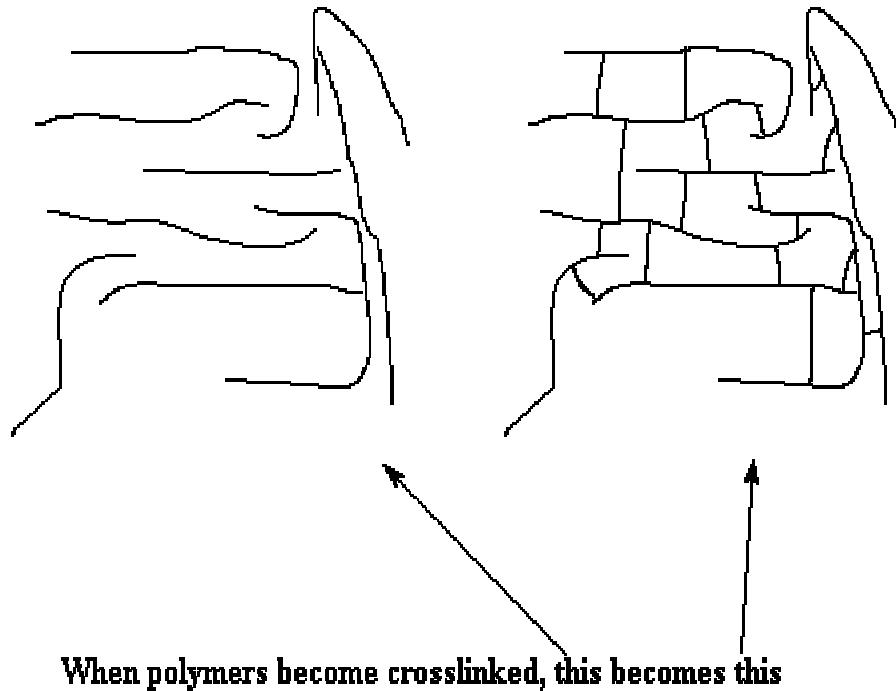


Figure 3. How polymers appear once they are crosslinked.

4. Embedded Atom Method (EAM)

The motions of individual molecules are best computed through molecular dynamics simulations. The energy and pressure of an equilibrium system are best seen through the use of these simulations. Temperature and density are the terms used to express energy and pressures. The temperature and density are instrumental in obtaining the thermodynamics of a system. The energy of a system is obtained by reversing the process described above. This scheme is called the embedded atom method (EAM) [5]. As pointed out by Daw in another context [6], the electron density uniquely specifies the energy of a system of atoms. With the uses of numerical methods, the forces can be determined from the system's energy as well as the thermodynamic properties of the material. The energy of a system can be represented by the EAM as such [6]:

$$E_{tot} = E_{kin} + E_{pot} \text{ or } E_{tot} = \sum_i E_{ee}(\rho_{h,i}) + \frac{1}{2} \sum_{i,j} \phi_{ij}(r_{ij}),$$

where $\rho_{h,i}$ is the total electron density seen by atom i due to the rest of the atoms in the system, E_{ee} is the embedding energy for placing an atom into that electron density and ϕ_{ij} is the short range pair interaction representing the core-core repulsion of atoms i and j separated by distance r_{ij} .

D. OBJECTIVES

In the last decade, a tremendous amount of attention has been dedicated to the development of polymeric blends. The production of materials with tailor made properties may be constructed with the use of these blends. This in turn may offer the development of completely new polymeric materials [7]. Analyzing and predicting polymer properties using atomistic simulations are crucial in the production of materials. Mechanical behavior, cohesion, permeability, and miscibility are all critical to the success of polymeric materials in technological applications. Polymer scientists seek to establish the connection between such properties, and the microscopic and mesoscopic structure of the polymers. The method used by scientist is atomistic simulation where a sample containing a few thousand atoms is a characteristic of the bulk system, and relaxation times for the property of interest are under a nanosecond.

Studying polymers to enhance the material properties of structures requires a model to predict the behavior of molecules. In particular, this thesis examines how the modulus of rigidity changes with density, and with a crystalline structure embedded in polymeric chains. This study uses microscopic principals to examine the molecular dynamics simulations. Scientists that have approached this study have all agreed that the polymer properties substantially deviate from the behavior in the bulk when closer to the solid interface [8-10]. Specifically, this thesis evaluates how many molecules per given chain are necessary for homogeneous behavior to occur.

II. PRE-PROCESSOR

A. INTRODUCTION

The contents of this chapter describe the construction of a molecular model. The goal is to randomly generate polymer chains within a cube and determine how many molecules per given chain are necessary to produce homogenous behavior. Computer simulations were used to focus on randomly dispersed particles in 3-D space. These simulations contained different volumes as well as polymers with different lengths, $N = 5 \dots 45$ with unit multiples of five molecules in a chain. The 3-D models of polymers were used to create structures that properly represent real molecules, thus, providing various construction and analysis strategies. Figure 4. shows a simulation with twelve polymer chains extending both in the x and y directions and two chains in the z direction.

With the use of crosslinking potential systems, molecular dynamics simulations were conducted in the three-dimensional polymeric matrix state. The simulations emphasize the relation between the correlation volume of a space, and the concentration of the random particles.

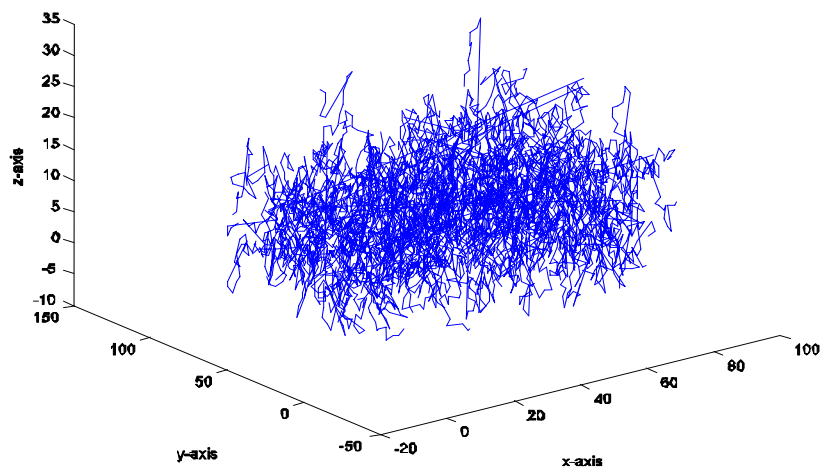


Figure 4. Composite material with particles randomly dispersed in a space volume of 90X90X15.

B. MOLECULAR MODEL

The interest lies in using the simplest molecular model possible that allows determination of the underlying physical phenomena of homogeneous behavior between the polymers. Polymer chains are typically long in nature. Theoretical models are based on interacting sites of the molecule connected by rods. A program was written to represent them in a similar manner to common theoretical models and address the details of the interactions between chain atoms as well as the nature of the solvent.

1. Chain Structure

As stated by Rapaport, the simplest model attempts to represent the individual monomers of the polymer and the bonds that link them into chains [11]. Monomers can be simple atoms modeled using a soft-sphere potential and the attractive interaction between chain neighbors can produce the limited length variation [11]. The chains are totally flexible with regards to the limits set by the repulsive potential. To control the interaction regulating the separation of the next-nearest neighbors, a degree of stiffness has to be included.

The model produced in this study was based on Rapaport's description of flexible molecules [11]. All pairs of atoms maintain an attractive interaction between each pair of adjacent bonded atoms. The force on particle i due to particle j , \mathbf{F}_{ij} , is of the form:

$$F_{ij} = -\frac{\partial U_{LJ}(r_{ij})}{\partial \vec{r}_i} = -\frac{\partial U_{LJ}(r_{ij})}{\partial r_{ij}} \frac{\partial r_{ij}}{\partial \vec{r}_i}$$

and acts along the vector joining the two particles.

2. Interaction

Forces between the non-bonded atoms belonging to the same chain must be taken into consideration. To compensate, the atoms belonging to the same chain must have identical atom identifications, the distance between molecules within the polymer equally spaced, and a tolerance set, for the allowable minimum distance between any two atoms.

3. Initial State

The selection of a monomer was at random and all other particles within a given distance of this particle were identified. The next random particle was connected to the first by the same potential used for the chain construction. The atoms of each chain must be positioned so that the bond lengths are all within their permitted ranges, and there are no overlapping of atoms either of the same or different chains. The added crystalline structure is organized as a face centered cubic (FCC) lattice, which the already existing chains positioned, to allow for wraparound.

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III. MOLECULAR DYNAMICS PROGRAMS

A. INTRODUCTION

Molecular dynamics is a technique that uses computers to solve the classical equations of motion for a system of atoms or molecules. A system of N particles interacts through a potential to determine the system's evolution through time. From the microscopic state of the system, i.e. particle positions and momenta, macroscopic properties such as pressure and energy can be evaluated.

In this chapter, descriptions of the MD program components for an atomic system at equilibrium are discussed.

B. SPACING

Molecules formed using this MATLAB program which is contained in Appendix A, were first confined to a cube with set dimensions in the x , y , and z directions. For the construction of the polymer chain, an allowable distance between molecules within the polymer was first established. All measurements during the construction were dimensionless. To ensure atoms were not too close or too far apart, an allowable tolerance input was set. After creating the foundation, the actual construction of the polymer chain began. For optimum results that were not too expensive, the number of polymer chains in the x and y directions were the same and the z direction was one third of the x direction's value. The number of molecules contained in each chain was chosen to be constant.

To determine the spacing in each direction, the lengths of the cube were divided by the number of polymer chains in the same direction. The total number of atoms contained in the cube was the product of the number of molecules in a chain and the number of polymer chains in the x , y , and z directions.

As far as the atomic structure is concerned, the bead-spring model was used. In essence, the bead-spring model simulates the hydrodynamic properties of a chain macromolecule. These chains consist of a sequence of beads, each of which offers hydrodynamic resistance to the flow of the surrounding medium. The beads are

connected to each other by a spring which does not contribute to the frictional interaction. However, the spring is responsible for the elastic and deformational properties of the chain. The mutual orientation of the springs is random.

For this project, each bead, or mapping point, represented a specific monomer. This required a fixed distance of the beads along the backbone, bond angles around the backbone, and torsion states around the bead-bead connection to be held constant.

A loop was generated to account for the individual atoms and their physical location. To initiate the chain creation, the first atom's position was generated. The remainder of the atoms along the chain was randomly generated. During the random generation, the atoms' positions were checked to verify if they were within the tolerance. Figures (5) and (6) show the results of the generation. The first 25 atoms of the generated polymers are contained in Tables (2) and (3). The program was run an additional two consecutive times with no changes.

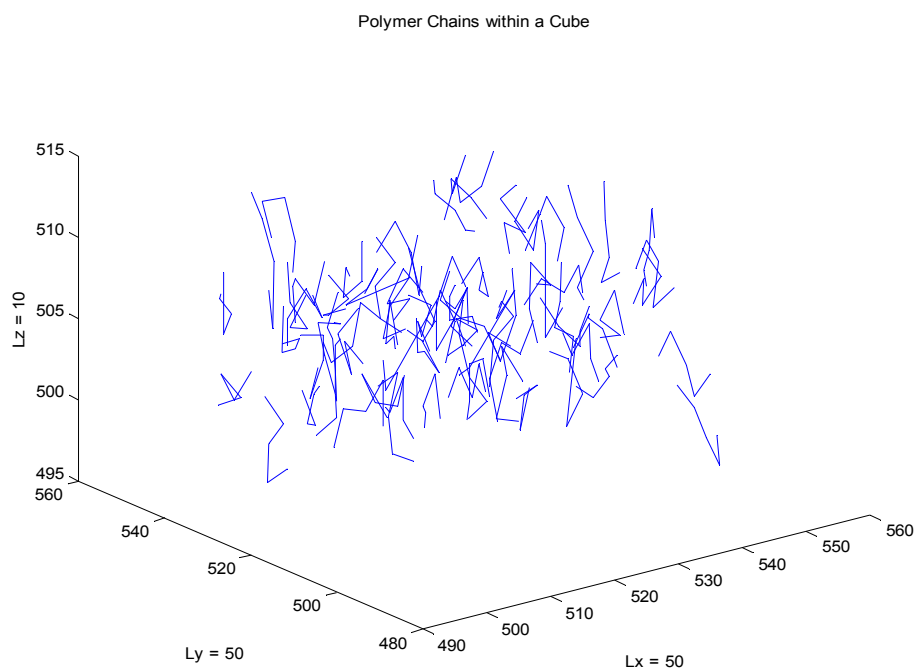


Figure 5. First iteration of random generated polymers with center (500, 500, 500)

| Atom | x | y | z | Atom ID |
|------|-----------|-----------|-----------|---------|
| 1.0 | 504.97609 | 504.48560 | 502.45171 | 101.0 |
| 2.0 | 502.59076 | 503.47293 | 503.96324 | 101.0 |
| 3.0 | 501.99942 | 502.42032 | 506.70957 | 101.0 |
| 4.0 | 499.67814 | 501.97644 | 504.86170 | 101.0 |
| 5.0 | 497.54537 | 500.01099 | 505.62873 | 101.0 |
| 6.0 | 512.37460 | 503.06179 | 502.99996 | 102.0 |
| 7.0 | 514.23613 | 505.30829 | 503.69847 | 102.0 |
| 8.0 | 515.55628 | 507.07712 | 505.73033 | 102.0 |
| 9.0 | 515.60933 | 504.13545 | 506.31661 | 102.0 |
| 10.0 | 516.83033 | 504.54918 | 503.84920 | 102.0 |
| 11.0 | 520.65245 | 503.22435 | 502.09824 | 103.0 |
| 12.0 | 518.28503 | 505.05995 | 502.25920 | 103.0 |
| 13.0 | 519.70948 | 504.65179 | 504.86771 | 103.0 |
| 14.0 | 518.02407 | 503.33075 | 506.96872 | 103.0 |
| 15.0 | 522.95581 | 505.88808 | 504.01570 | 103.0 |
| 16.0 | 528.90952 | 502.40789 | 503.49247 | 104.0 |
| 17.0 | 531.73406 | 502.57428 | 502.49534 | 104.0 |
| 18.0 | 532.67934 | 500.17630 | 504.03032 | 104.0 |
| 19.0 | 533.97179 | 502.88360 | 504.03933 | 104.0 |
| 20.0 | 533.87432 | 500.11420 | 505.18864 | 104.0 |
| 21.0 | 537.16469 | 505.11076 | 503.50474 | 105.0 |
| 22.0 | 535.65462 | 506.06503 | 505.91494 | 105.0 |
| 23.0 | 532.89417 | 505.52865 | 506.96004 | 105.0 |
| 24.0 | 531.48535 | 502.96331 | 507.61903 | 105.0 |
| 25.0 | 529.87864 | 504.46564 | 505.57906 | 105.0 |

Table 2 First 25 Atoms of Figure (5)

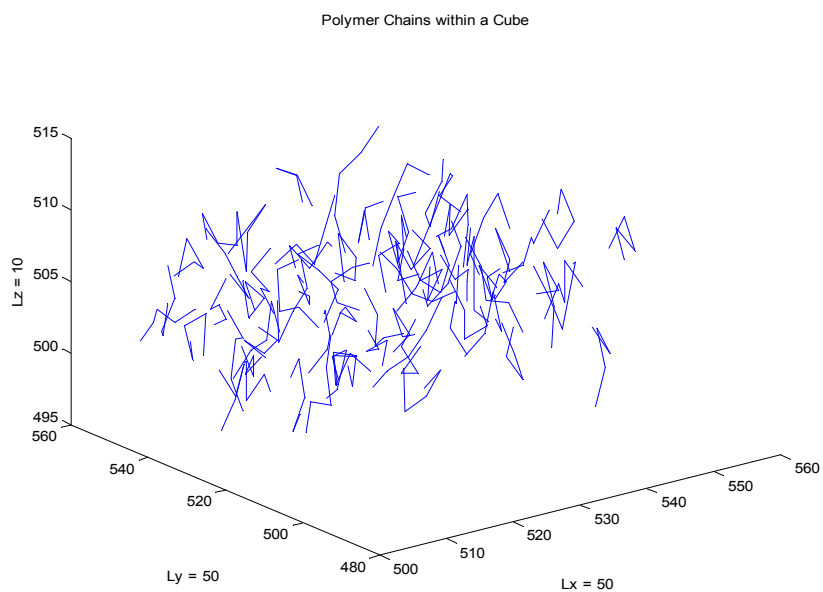


Figure 6. Second iteration of the same random generated polymers with center (500, 500, 500)

| Atom | x | y | z | Atom ID |
|------|-----------|-----------|-----------|---------|
| 1.0 | 505.92154 | 504.03955 | 502.51789 | 101.0 |
| 2.0 | 505.84193 | 501.20613 | 503.50041 | 101.0 |
| 3.0 | 507.36395 | 501.26903 | 506.08488 | 101.0 |
| 4.0 | 506.81471 | 504.13124 | 505.37349 | 101.0 |
| 5.0 | 508.49709 | 505.65925 | 503.41522 | 101.0 |
| 6.0 | 513.94974 | 505.92256 | 502.12355 | 102.0 |
| 7.0 | 516.62952 | 507.08035 | 502.81516 | 102.0 |
| 8.0 | 518.82241 | 505.27689 | 503.78403 | 102.0 |
| 9.0 | 521.22632 | 504.63156 | 505.45879 | 102.0 |
| 10.0 | 522.71982 | 503.34969 | 507.72291 | 102.0 |
| 11.0 | 520.31054 | 503.88540 | 501.52354 | 103.0 |
| 12.0 | 523.12281 | 504.38051 | 502.44330 | 103.0 |
| 13.0 | 522.22704 | 506.48774 | 500.50496 | 103.0 |
| 14.0 | 519.43758 | 507.16691 | 499.63453 | 103.0 |
| 15.0 | 519.57860 | 507.70756 | 502.58203 | 103.0 |
| 16.0 | 527.12844 | 505.03416 | 502.87971 | 104.0 |
| 17.0 | 529.22768 | 503.53851 | 504.41470 | 104.0 |
| 18.0 | 530.24602 | 503.15056 | 507.20978 | 104.0 |
| 19.0 | 531.05067 | 502.23159 | 504.46970 | 104.0 |
| 20.0 | 531.71551 | 505.11960 | 504.93591 | 104.0 |
| 21.0 | 535.71797 | 504.87248 | 503.58545 | 105.0 |
| 22.0 | 533.79039 | 505.06657 | 505.87603 | 105.0 |
| 23.0 | 531.21955 | 506.59679 | 506.09787 | 105.0 |
| 24.0 | 531.74211 | 508.66777 | 508.20452 | 105.0 |
| 25.0 | 529.78274 | 509.45735 | 510.33464 | 105.0 |

Table 3 First 25 Atoms of Figure (6)

C. POTENTIALS

The interactions between the polymers and atoms lead to prediction of the large-scale bulk properties of material. This molecular dynamics program uses the Lennard Jones (LJ) potential method to evaluate molecule interactions between the polymers and atomic atoms. The LJ potential is an effective potential that describes the interaction between two uncharged molecules or atoms.

The Lennard-Jones potential is mildly attractive as two uncharged molecules or atoms approach one another from a distance, but strongly repulsive when they approach too close. At equilibrium, the pair of atoms or molecules tends to go toward a separation corresponding to the minimum of the LJ potential. The strong *close-in* repulsion between atoms or molecules is understandable, resulting from mutual deformation of their structures (one atom cannot diffuse through another). The mild attraction at larger distances is due to the induced dipole-dipole moment interaction of the particles.

1. Polymers

As stated previously, the LJ potential was used to ensure self avoidance of polymers. The general form is:

$$U_{LJ}(r_{ij}) = \begin{cases} 4\epsilon \left[\left(\frac{\sigma}{r_{ij}} \right)^{12} - \left(\frac{\sigma}{r_{ij}} \right)^6 + \frac{1}{4} \right] & \left\{ \begin{array}{l} r_{ij} < 2^{1/6} \sigma \\ r_{ij} \geq 2^{1/6} \sigma \end{array} \right\} \\ 0 & \end{cases}$$

where ϵ and σ , are defined as the energy at the minimum in potential and the distance to zero in potential, respectively and r_{ij} is the inter-atomic distance.

The following formula was used to compensate for the added attractive potential between neighboring atoms:

$$U_{nn}(r_{ij}) = \begin{cases} -\frac{1}{2} k R_o^2 \ln \left[1 - \left(\frac{r_{ij}}{R_o} \right)^2 \right] & \left\{ \begin{array}{l} r_{ij} < R_o \\ r_{ij} \geq R_o \end{array} \right\} \\ \infty & \end{cases}$$

with $R_o = 1.5\sigma$ and $k=30\epsilon/\sigma^2$. By incorporating this method, polymers are prevented from passing through each other [4].

2. Metallic Atoms

The embedded atomic potential as described in section I-C.4.a was used for the metallic atoms. The foundation of the embedded atom method (EAM), based on the quasi-atom concept, is the realization that the cohesive energy of a metallic system can be expressed in terms of embedding energies. Daw *et al.* [12] have resorted to empiricism by fitting the embedding function and pair interaction to basic bulk properties, e.g., lattice constant, cohesive energy, elastic constants, and vacancy formation energy. Figure 7 shows the creation of a polymer with an aluminum core.

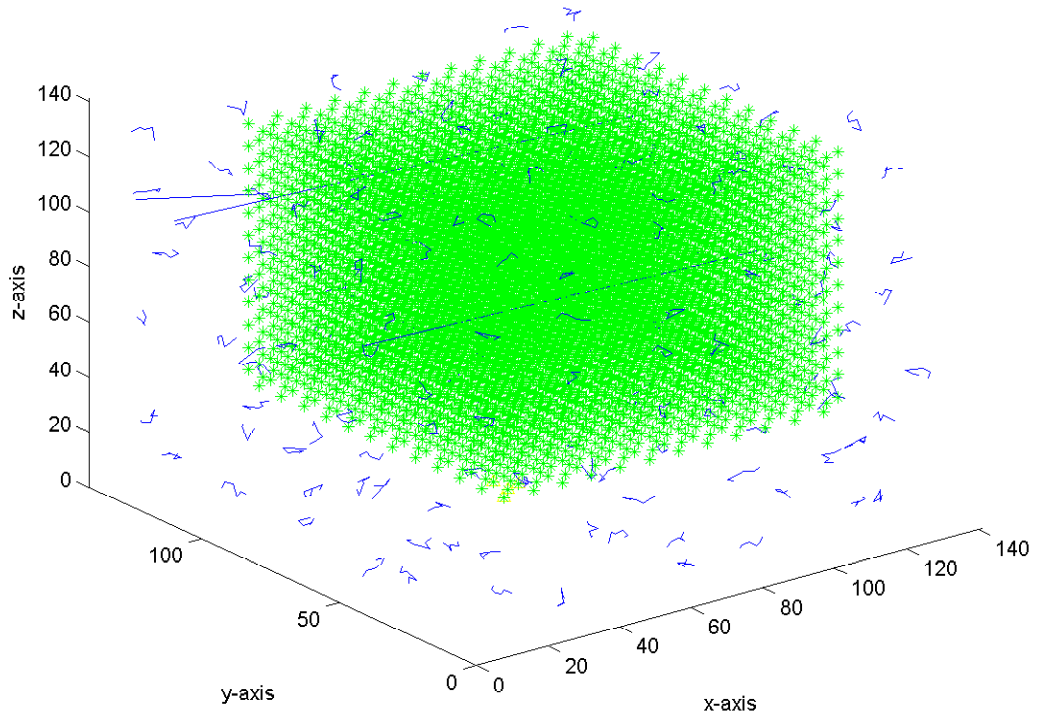


Figure 7. Random Generate Polymer with Aluminum center contained in a Volume = 141X141X141. Number of polymers in each chain in x, y, and z direction is 6 with 6 beads in each chain. Total number of atoms in structure is 8160 atoms.

D. MOLECULE INTERACTION

The Lennard-Jones potential is used to determine the forces acting on each particle. The forces are used in solving the particle trajectories as they evolve in time. In this program, the potential file contains the following information: atomic number, atomic mass, lattice spacing, potential cut-off range for each atom, grid of inter-atomic force, grid of atom electron density and the spherically averaged atomic density [12]. To determine the embedding energy of each atom, the inter-atomic force is interpolated for each atom site and multiplied with the atom density. The cohesion energy of the system is determined by summing the embedding energy over all the host atoms. Lastly, the force is computed by multiplying the electron density at each atom with the embedded energy.

E. MODEL

Within the model created, the number of monomers (beads) on each chain may be changed by the user. This input is multiplied by the number of polymers chains in the x, y, and z directions to determine the number of polymers in the system.

Each system was equilibrated to an average dimensionless temperature of 300 and a time step equal to 0.01. This process was completed through a constant energy molecular dynamics code where the user was required to enter the number of atoms contained in the system.

With the use of the equations contained in section III-C above, the polymer chains were created and cross-linking introduced. A molecule was selected at random and then connected to another random molecule within the same polymer chain. A standard distance was used for the molecules along with a combination of the potentials for polymers described above. Molecules contained in the same chain were only linked once, and no cross-linking of neighboring atoms was permitted.

F. AUTO-CORRELATION

All of the viscometric functions are derived from elements of the stress tensor. The stress tensor can be determined from the pressure tensor, so only one of these need

be calculated by the program. In an equilibrium molecular dynamics simulation, Newton's equations describing the motion of the atoms in the model system are solved as a function of time. The viscosity η is then given as an integral of the stress-stress autocorrelation functions determined during the simulation,

$$\eta = \frac{V}{k_B T} \lim_{\tau \rightarrow \infty} \frac{1}{\tau} \int_0^\tau dt \langle P_{xy}(t) P_{xy}(0) \rangle$$

where V is the volume of the system, k_B is Boltzmann's constant, T is temperature, and t is time. The quantity $P_{xy}(t)$ is the value of the xy component of the traceless symmetric stress tensor at time t , and so $P_{xy}(t)P_{xy}(0)$ is the stress-stress autocorrelation function measured during the course of the simulation.

IV. RESULTS AND DISCUSSION

A. INTRODUCTION

In this chapter the results of all the simulations are presented and discussed. Before these simulations were carried out, extensive work was required to ensure the program functioned correctly.

Dimensionless units were used to compute the stress tensor in the xy , yz , and xz directions. Several variables remained constant throughout each simulation to observe the polymer behavior. The temperature remained constant at a rate of 300 with a time step of 0.01. The number of atoms (NATOMS) was initially computed by the number of beads or molecules in a chain multiplied by the number of polymer chains in each direction. The density was then calculated by dividing the NATOMS by the cube's volume.

All simulations ran a minimum of three times. An average of the results was recorded and plotted. In all of the simulations completed, there is a noticeable homogeneous trend. These results are presented in the sections to follow.

B. VARYING DENSITY AND VOLUME PROPORTIONALLY

The first simulation required proportionally varying the x and y dimensions of the cube along with the number of atoms in the same directions. The cube length in the z direction was set to a constant and the number of polymer chains extending in this direction was two. The number of monomers in a chain remained constant at 20. We noted that the normalized shear modulus approaches a constant value, as seen in Figure 8 when NATOMS becomes more than 8000.

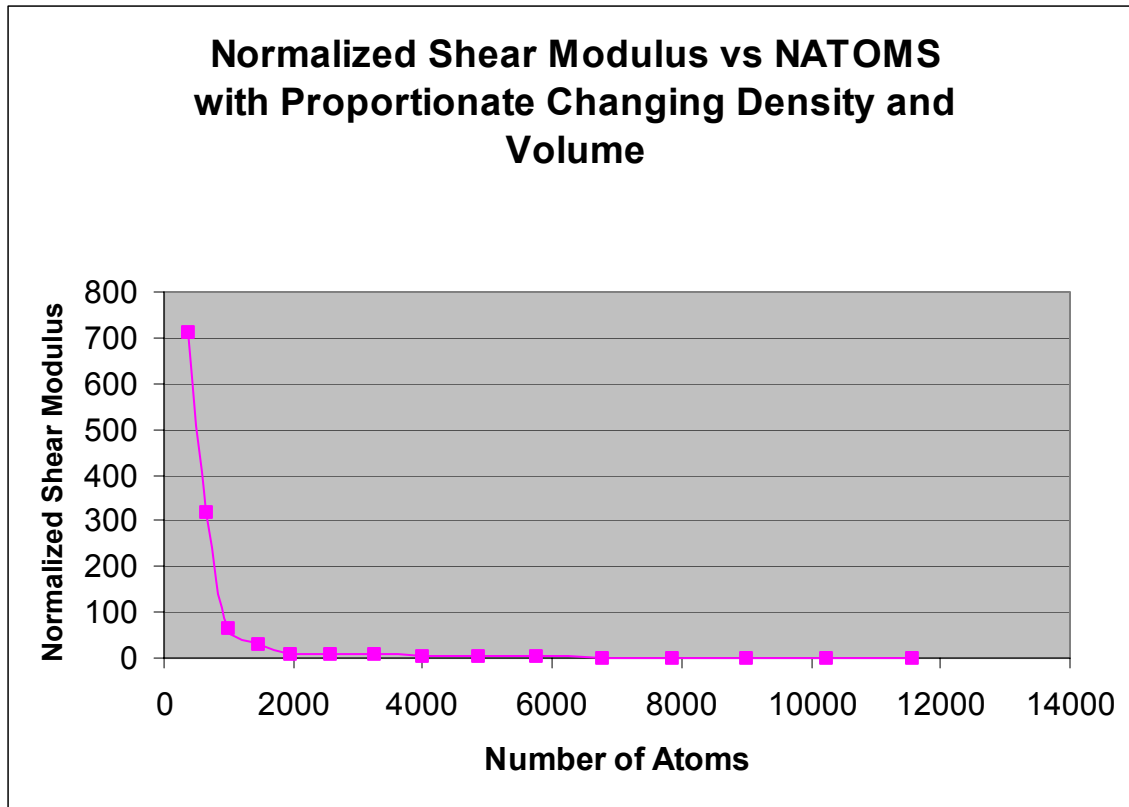


Figure 8. Plot of the normalized shear modulus as a result of proportionally varying the density with the volume of the cube.

C. CONSTANT VOLUME

During this simulation, the volume was held constant, and the number of monomers per chain was held at 20. The number of polymer chains which extended in the z direction remained constant at $N_z=2$; however, the x and y directions were increased by one unit starting from $N_x=N_y=3$ after a series of runs were completed. After the total number of atoms becomes about 9000, the shear modulus remains roughly constant as seen in Figure 9.

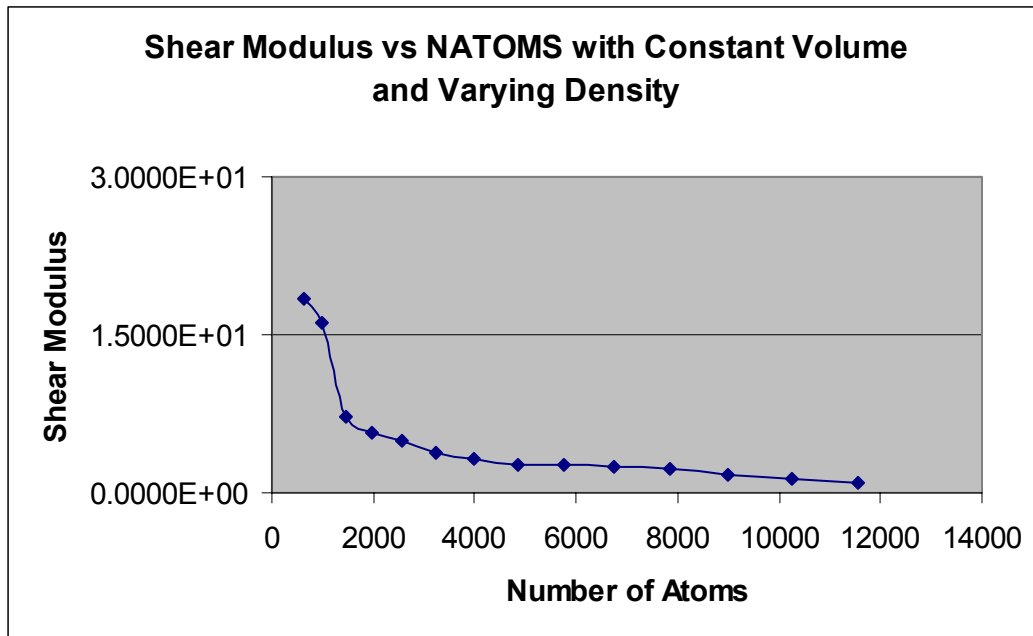


Figure 9. Plot of the normalized shear modulus determined from a cube of constant volume (112.5X112.5X15) as a function of varying density.

D. CONSTANT VOLUME AND DENSITY WITH VARIANCE IN NUMBER OF MOLECULES PER CHAIN

This simulation required holding both the volume and density constant. The one varying parameter was the number of monomers per given chain (N). The increments were in units of 5 beginning with N=5...45. The results show that the normalized shear modulus begins to approach a constant value as NATOMS becomes more than 8000 as seen in Figure 10.

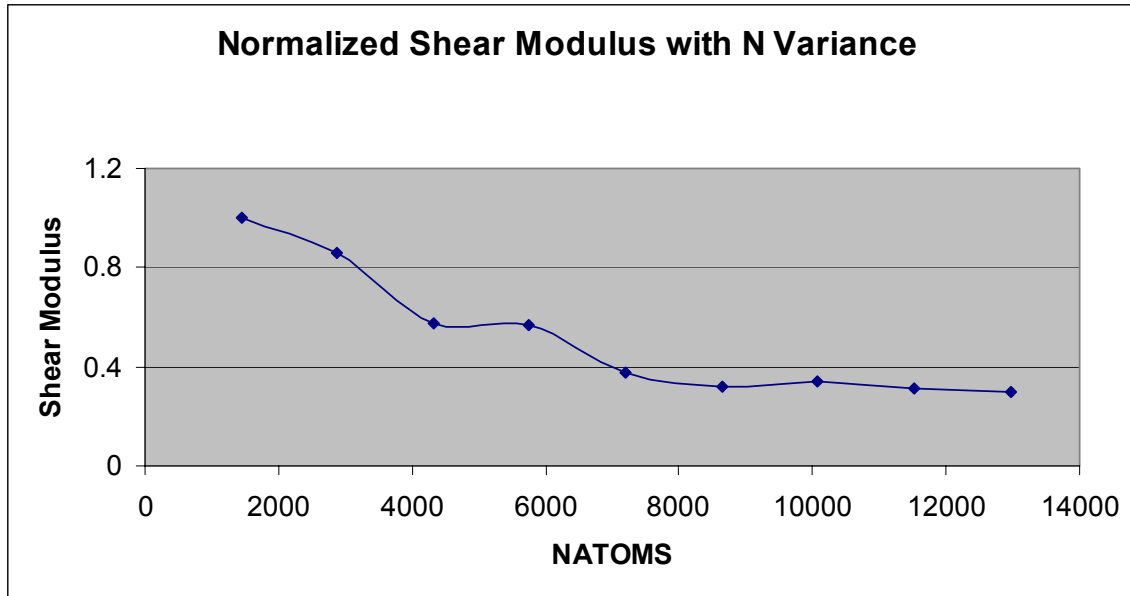


Figure 10. Plot of the normalized shear modulus determined from a cube with constant volume and polymer density as a function of molecules variance.

E. CONSTANT VOLUME WITH METALLIC CORE

A face center cube (FCC) structure was inserted in the center of a cube with a constant volume. The FCC was used to simulate the characteristics of aluminum. There were six polymer chains extending in each direction with a variance in the number of monomers per given chain for the first simulation. The varying parameters for this simulation included the size of the FCC and the number of polymers interacting with this metallic structure. Thus, the number of monomers per given chain decreased proportionally with the expansion of the metallic structure to maintain a constant density.

Ideally, this simulation was created to represent a composite material. As the metallic core size increased, the polymers' space became more confined due to the constant volume of the cube. This means the volume fraction of the metallic particle increases in a polymer composite. As shown in Figure 11, the normalized shear modulus continuously increases along with the increasing size of the metallic core.

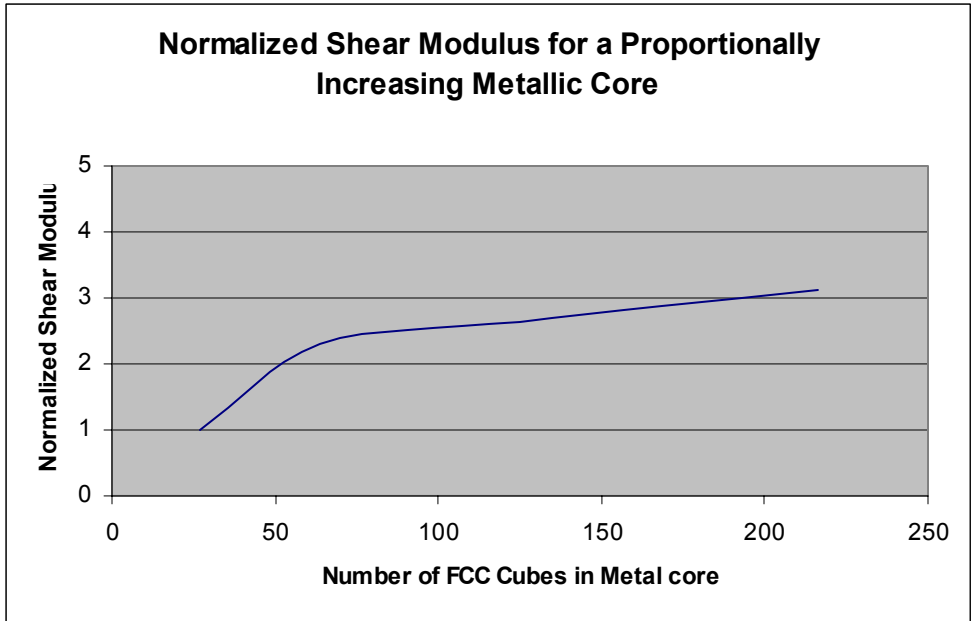


Figure 11. Plot of the average normalized shear modulus for a cube with a constant volume and increasing metallic core size under constant polymer density.

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V. CONCLUSIONS AND RECOMMENDATIONS

A. CONCLUSIONS

Atomistic simulations have been carried out on a wide range of polymers. The subject of scale of microstructure on bulk properties is the basis of this study for polymer matrix nano-composites. Extremely small, rigid particles can be distributed in a soft matrix to engineer specific physical properties. The purpose of this is to provide insights on theoretical methods usage which describes the mechanical properties (stress/strain performance) of nano-materials composed of polymers and metallic structures. Ongoing experimental studies are designed to understand the role of the nano-scale particles in changing the composite mechanical properties. Theoretical modeling of nano-mechanical interactions is applied to examine a variety of unique small scale effects.

The goal of this thesis was to develop insights as to how a molecular level structure is connected to the bulk properties of materials assuming homogeneity. A molecular dynamics program was used to take a closer look at the effects of different sizes, densities, and numbers of molecules per chain on the shear moduli.

Based on the numerous simulations conducted, a common occurrence emerged across the board. The normalized shear modulus decreased to a constant value as the total number of atoms in the model increased. The results show that approximately 8000 or more monomers are needed in order to represent the polymer behavior, regardless of number of polymer chains, number of monomers per chain, or density of the polymers. For the particulate composite, the shear modulus increased along with the size of the metallic particle (i.e. particle volume fraction). In this simulation, if the number of polymers is small, the composite shear modulus could not be determined properly. Thus, it is critical to contain a minimum number of polymers in the molecular dynamic simulation in order to obtain reliable predictions.

B. RECOMMENDATIONS

This project is an important issue that can be very beneficial for polymer material design. Engineers believe the role of polymer composites is rapidly growing due to their

strength, lightweight, chemical stability and tailor-ability [13]. This thesis provides baseline information for obtaining information on the mechanical properties of polymers and bulk material. One important issue that requires further investigation is the cross-linking density relationship. In this thesis, the cross-linking density remained constant throughout all simulations.

Another area for research to consider is the function responses with different types of metals. This will prove beneficial in the creation and modification of other composites.

APPENDIX A - MATLAB CODE

A. GENERATION OF POLYMERS

```
clc;
clf;
clear;

% center position of the polymer unit
xc=0; yc=0; zc=0;

% dimensions of cube
Lx=28.2*5;
Ly=28.2*5;
Lz=28.2*5;

%distance between molecules within polymer
lc=2.0;

% allowable minimum distance between any two atoms
toler = 2.0;

%Increments in each direction
Nx=6; % no. of polymer chains in x-dir
Ny=6; % no. of polymer chains in y-dir
Nz=6; % no. of polymer chains in z-dir

% number of molecules (bead) in a chain
N=125;

%Spacing in each direction
dx = Lx/Nx;
dy = Ly/Ny;
dz = Lz/Nz;

%FCC Parameters

NUNIT1=4;
NUNIT2=NUNIT1;
NUNIT3=NUNIT1;

DIST = 4.05;

Lx1=(2/5*Lx)+dx/8;
Ly1=(2/5*Ly)+dy/8;
Lz1=(2/5*Lz)+dz/8;
Lx2=(3/5*Lx)+dx/8;
Ly2=(3/5*Ly)+dy/8;
Lz2=(3/5*Lz)+dz/8;

% Lx1=(Lx-(NUNIT2/2))/2 -(NUNIT2*DIST)/2 + dx/8;
% Ly1=Lx1;
```

```

% Lz1=Lx1;
% Lx2=(Lx-(NUNIT2/2))/2 + (NUNIT2*DIST)/2 + dx/8;
% Ly2=Lx2;
% Lz2=Lx2;

Lx11=Lx1+dx/10;
Ly11=Ly1+dy/10;
Lz11=Lz1+dz/10;

NATOM=0;
NMOLE=0;

%Loop for seed points for molecular positions
ij=0;
dummy=0;
for k=1:Nz
    for j=1:Ny
        for i=1:Nx
            xx=(i-1)*dx + dx/2 + xc;
            yy=(j-1)*dy + dy/2 + yc;
            zz=(k-1)*dz + dz/2 + zc;
            if ( (xx>Lx1 & xx<Lx2) & (yy>Ly1 & yy<Ly2) & (zz>Lz1 & zz<Lz2) );
                dummy=dummy+1;
            else
                NMOLE=NMOLE+1;
                ij=ij+1;
                x(ij)=(i-1)*dx + dx/2 + xc;
                y(ij)=(j-1)*dy + dy/2 + yc;
                z(ij)=(k-1)*dz + dz/2 + zc;
            end
        end
    end
end
end

NATOM=NMOLE*N

figure(1)

%Create FCC

%    Assign initial positions to id 1 for the first 256 atoms
%    based on face-centered cubic lattice total atoms
id=1;
%....    set lattice distance based on cube of side + CUBE

    jatom = 1;
%    NUNIT1=4;
%    NUNIT2=4;
%    NUNIT3=4;
%    DIST = 4.05;
    atomid(jatom) = id;
%....    assign positions of first four atoms
    xnew(jatom) = Lx11 ;
    ynew(jatom) = Ly11 ;
    znew(jatom) = Lz11 ;

```

```

xnew(jatom+1) = Lx11;
ynew(jatom+1) = Ly11+DIST;
znew(jatom+1) = Lz11+DIST;
xnew(jatom+2) = Lx11+DIST;
ynew(jatom+2) = Ly11;
znew(jatom+2) = Lz11+DIST;
xnew(jatom+3) = Lx11+DIST;
ynew(jatom+3) = Ly11+DIST;
znew(jatom+3) = Lz11;
plot3(xnew,ynew,znew,'y^')
hold on
% .... replicate first four positions over NUNITS
jatom=0;
for I=1: NUNIT1
    for J=1: NUNIT2
        for K=1: NUNIT3
            for IJ=1:4
                xnew(IJ+jatom) = xnew(IJ) + 2*DIST*(K-1);
                ynew(IJ+jatom) = ynew(IJ) + 2*DIST*(J-1);
                znew(IJ+jatom) = znew(IJ) + 2*DIST*(I-1);
                atomid(IJ+jatom)=id;
            end
            jatom=jatom+4;
            plot3 (xnew,ynew,znew,'g*')
            hold on
        end
    end
end
end

NMET=jatom
NATOM_TOTAL=(NATOM+NMET)
%Generate Random numbers for specified point
id=20;
for imole=1:NMOLE
    % create the first atom's position of each chain
    id=id+1;
    x1=x(imole); y1=y(imole); z1=z(imole);
    rn=rand(1,3);
    rn1(1,1)=rn(1,1)-0.5; rn1(1,2)=rn(1,2)-0.5; rn1(1,3)=rn(1,3)-0.5;
    jatom = jatom + 1;
    atomid(jatom)=id;
    xnew(jatom)=x(imole) + dx*rn1(1,1)*0.5;
    ynew(jatom)=y(imole) + dy*rn1(1,2)*0.5;
    znew(jatom)=z(imole) + dz*rn1(1,3)*0.5;

    % create the remaining (N-1) atoms' positions
    for iatom=2:N
        iflag=0;
        jatom = jatom + 1;
        rn=rand(1,3); rn1(1,1)=rn(1,1)-0.5; rn1(1,2)=rn(1,2)-0.5; rn1(1,3)=rn(1,3)-0.5;
        mag=sqrt(rn1(1,1)^2 + rn1(1,2)^2 + rn1(1,3)^2); %magnitude
        uvx=rn1(1,1)/mag;
        uvy=rn1(1,2)/mag;
        uvz=rn1(1,3)/mag;
        atomid(jatom)=id;
        xnew(jatom) = xnew(jatom-1) + uvx*lc;
    end
end

```

```

ynew(jatom) = ynew(jatom-1) + uvy*lc;
znew(jatom) = znew(jatom-1) + uvz*lc;

while((xnew(jatom)>Lx1 & xnew(jatom)<Lx2) & ...
      (ynew(jatom)>Ly1 & ynew(jatom)<Ly2) & ...
      (znew(jatom)>Lz1 & znew(jatom)<Lz2))

    iflag = iflag+1;

    if (iflag > 100)
        break
    end

    rn=rand(1,3); rn1(1,1)=rn(1,1)-0.5; rn1(1,2)=rn(1,2)-0.5; rn1(1,3)=rn(1,3)-0.5;
    mag=sqrt(rn1(1,1)^2 + rn1(1,2)^2 + rn1(1,3)^2); %magnitude
    uvx=rn1(1,1)/mag;
    uvy=rn1(1,2)/mag;
    uvz=rn1(1,3)/mag;
    atomid(jatom)=id;
    xnew(jatom) = xnew(jatom-1) + uvx*lc;
    ynew(jatom) = ynew(jatom-1) + uvy*lc;
    znew(jatom) = znew(jatom-1) + uvz*lc;
end
end

%Check whether two atoms' positions are within the tolerance

if (imole==1)
    for ipatom=2:jatom
        testid=1;
        iter=1;
        while (testid > 0.1 & iter <= 50 )
            iter=iter+1;
            testid=0;
            for itest=1:(ipatom-1)
                dist = sqrt((xnew(ipatom)-xnew(itest))^2+(ynew(ipatom)-
ynew(itest))^2+(znew(ipatom)-znew(itest))^2);
                if dist < toler;
                    testid=testid+1;
                end
            end
        end

        if (testid > 0.1)
            rn=rand(1,3); rn1(1,1)=rn(1,1)-0.5; rn1(1,2)=rn(1,2)-0.5; rn1(1,3)=rn(1,3)-0.5;

            % Magnitude
            mag=sqrt(rn1(1,1)^2 + rn1(1,2)^2 + rn1(1,3)^2);
            uvx=rn1(1,1)/mag;
            uvy=rn1(1,2)/mag;
            uvz=rn1(1,3)/mag;
            xnew(ipatom) = xnew(ipatom-1) + uvx*lc;
            ynew(ipatom) = ynew(ipatom-1) + uvy*lc;
            znew(ipatom) = znew(ipatom-1) + uvz*lc;
            iflag=0;
            while((xnew(jatom)>Lx1 & xnew(jatom)<Lx2) & ...
                  (ynew(jatom)>Ly1 & ynew(jatom)<Ly2) & ...

```

```

(znew(jatom)>Lz1 & znew(jatom)<Lz2))

iflag=iflag+1;

if (iflag > 100)
    break
end
rn=rand(1,3); rn1(1,1)=rn(1,1)-0.5; rn1(1,2)=rn(1,2)-0.5; rn1(1,3)=rn(1,3)-0.5;
mag=sqrt(rn1(1,1)^2 + rn1(1,2)^2 + rn1(1,3)^2); %magnitudo
uvx=rn1(1,1)/mag;
vy=rn1(1,2)/mag;
vz=rn1(1,3)/mag;
atomid(jatom)=id;
xnew(ipatom) = xnew(ipatom-1) + uvx*lc;
ynew(ipatom) = ynew(ipatom-1) + vy*lc;
znew(ipatom) = znew(ipatom-1) + vz*lc;
end
end

end
if (iter > 49)
    break
end
end
else
for ipatom=(imole-1)*N+1:jatom
    testid=1;
    iter=1;
    while (testid > 0.1 & iter < 50 )
        iter=iter+1;
        testid=0;
        for itest=1:(ipatom-1)
            dist = sqrt((xnew(ipatom)-xnew(itest))^2+(ynew(ipatom)-
ynew(itest))^2+(znew(ipatom)-znew(itest))^2);
            if dist < toler;
                testid=testid+1;
            end
        end
    end

if (testid > 0.1)
    rn=rand(1,3); rn1(1,1)=rn(1,1)-0.5; rn1(1,2)=rn(1,2)-0.5; rn1(1,3)=rn(1,3)-0.5;

%Magnitude
mag=sqrt(rn1(1,1)^2 + rn1(1,2)^2 + rn1(1,3)^2);

uvx=rn1(1,1)/mag;
vy=rn1(1,2)/mag;
vz=rn1(1,3)/mag;
xnew(ipatom) = xnew(ipatom-1) + uvx*lc;
ynew(ipatom) = ynew(ipatom-1) + vy*lc;
znew(ipatom) = znew(ipatom-1) + vz*lc;
iflag=0;

while((xnew(jatom)>Lx1 & xnew(jatom)<Lx2) & ...
(ynew(jatom)>Ly1 & ynew(jatom)<Ly2) & ...
(znew(jatom)>Lz1 & znew(jatom)<Lz2))

```



```

        iflag=iflag+1;

        if (iflag > 100)
            break
        end

        rn=rand(1,3); rn1(1,1)=rn(1,1)-0.5; rn1(1,2)=rn(1,2)-0.5; rn1(1,3)=rn(1,3)-0.5;
        mag=sqrt(rn1(1,1)^2 + rn1(1,2)^2 + rn1(1,3)^2); %magnititude
        uvx=rn1(1,1)/mag;
        uvy=rn1(1,2)/mag;
        uvz=rn1(1,3)/mag;
        atomid(jatom)=id;
        xnew(ipatom) = xnew(ipatom-1) + uvx*lc;
        ynew(ipatom) = ynew(ipatom-1) + uvy*lc;
        znew(ipatom) = znew(ipatom-1) + uvz*lc;
    end

    end
end
if (iter > 49)
    break
end
end
end
    irstart=jatom-N+1;
    iend=jatom;
    plot3(xnew(irstart:iend),ynew(irstart:iend),znew(irstart:iend))
    axis([0 Lx 0 Ly 0 Lz])
    xlabel('x-axis'); ylabel('y-axis'); zlabel('z-axis');
    hold on
end

for iatom=NMET:NATOM_TOTAL
    xxx=xnew(iatom); yyy=ynew(iatom); zzz=znew(iatom);

    if ( (xxx>Lx11 & xxx<Lx2) & (yyy>Ly11 & yyy<Ly2) & (zzz>Lz11 & zzz<Lz2))
        plot3(xxx,yyy,zzz,'ro');
    else
        % plot3(xxx,yyy,zzz,'o');
    end
end

hold off

fidin=fopen('molecule_grid.txt','w');
for ii=1:NATOM_TOTAL
    fprintf(fidin,'%5.1f          %12.5f          %12.5f          %12.5f          %10.1f\n',ii,xnew(ii),ynew(ii),znew(ii),atomid(ii));
end
fclose(fidin);

% center postion of the polymer unit

```

```

xc=0; yc=0; zc=0;

% dimensions of cube
Lx=28.2*5;
Ly=28.2*5;
Lz=28.2*5;

%distance between molecules within polymer
lc=2.0;

% allowable minimum distance between any two atoms
toler = 2.0;

%Increments in each direction
Nx=6; % no. of polymer chains in x-dir
Ny=6; % no. of polymer chains in y-dir
Nz=6; % no. of polymer chains in z-dir

% number of molecules (bead) in a chain
N=12;

%Spacing in each direction
dx = Lx/Nx;
dy = Ly/Ny;
dz = Lz/Nz;

%internal volume
Lx1=(1/5*Lx+1/4*28.2)+dx/8;
Ly1=(1/5*Ly+1/4*28.2)+dy/8;
Lz1=(1/5*Lz+1/4*28.2)+dz/8;
Lx2=(4/5*Lx-1/4*28.2)+dx/8;
Ly2=(4/5*Ly-1/4*28.2)+dy/8;
Lz2=(4/5*Lz-1/4*28.2)+dz/8;

Leng = Lx2-Lx1

Lx11=Lx1+dx/10;
Ly11=Ly1+dy/10;
Lz11=Lz1+dz/10;

%NATOM=N*Nx*Ny*Nz
%NMOLE=Nx*Ny*Nz;
NATOM=0;
NMOLE=0;

%Loop for seed points for molecular positions
ij=0;
dummy=0;
for k=1:Nz
    for j=1:Ny
        for i=1:Nx
            xx=(i-1)*dx + dx/2 + xc;
            yy=(j-1)*dy + dy/2 + yc;

```

```

        zz=(k-1)*dz + dz/2 + zc;
    if ( (xx>Lx1 & xx<Lx2) & (yy>Ly1 & yy<Ly2) & (zz>Lz1 & zz<Lz2) );
        dummy=dummy+1;
    else
        NMOLE=NMOLE+1;
        ij=ij+1;
        x(ij)=(i-1)*dx + dx/2 + xc;
        y(ij)=(j-1)*dy + dy/2 + yc;
        z(ij)=(k-1)*dz + dz/2 + zc;
    end
end
end
end
end

```

NATOM=NMOLE*N

figure(1)

%Create FCC

% Assign initial positions to id 1 for the first 256 atoms
 % based on face-centered cubic lattice total atoms

id=21;

jatom=0;

FCC = 260;

%... set lattice distance based on cube of side + CUBE

for i_mole=1:FCC

 jatom = jatom + 1;

 NUNIT1=4;

 NUNIT2=4;

 NUNIT3=4;

 DIST = 5.8*2;

% DIST = 17.625;

 atomid(jatom) = id;

%... assign positions of first four atoms

 xnew(jatom) = Lx11 ;

 ynew(jatom) = Ly11 ;

 znew(jatom) = Lz11 ;

 xnew(jatom+1) = Lx11;

 ynew(jatom+1) = Ly11+DIST;

 znew(jatom+1) = Lz11+DIST;

 xnew(jatom+2) = Lx11+DIST;

 ynew(jatom+2) = Ly11;

 znew(jatom+2) = Lz11+DIST;

 xnew(jatom+3) = Lx11+DIST;

 ynew(jatom+3) = Ly11+DIST;

 znew(jatom+3) = Lz11;

 plot3(xnew,ynew,znew,'y^')

 hold on

% ... replicate first four positions over NUNITS

for I=1: NUNIT1

 for J=1: NUNIT2

 for K=1: NUNIT3

 for IJ=1:4

 xnew(jatom+4) = xnew(IJ) + 2*DIST*(K-1);

```

        ynew(jatom+4) = ynew(IJ) + 2*DIST*(J-1);
        znew(jatom+4) = znew(IJ) + 2*DIST*(I-1);
    end
    plot3 (xnew,ynew,znew,'g*')
    hold on
end
end
end
end

end
%Generate Random numbers for specified point

for imole=1:NMOLE
    % create the first atom's position of each chain
    id=id+1;
    x1=x(imole); y1=y(imole); z1=z(imole);
    rn=rand(1,3);
    rn1(1,1)=rn(1,1)-0.5; rn1(1,2)=rn(1,2)-0.5; rn1(1,3)=rn(1,3)-0.5;
    jatom = jatom + 1;
    atomid(jatom)=id;
    xnew(jatom)=x(imole) + dx*rn1(1,1)*0.5;
    ynew(jatom)=y(imole) + dy*rn1(1,2)*0.5;
    znew(jatom)=z(imole) + dz*rn1(1,3)*0.5;

    % create the remaining (N-1) atoms' positions
    for iatom=2:N
        iflag=0;
        jatom = jatom + 1;
        rn=rand(1,3); rn1(1,1)=rn(1,1)-0.5; rn1(1,2)=rn(1,2)-0.5; rn1(1,3)=rn(1,3)-0.5;
        mag=sqrt(rn1(1,1)^2 + rn1(1,2)^2 + rn1(1,3)^2); %magnititude
        uvx=rn1(1,1)/mag;
        uvy=rn1(1,2)/mag;
        uvz=rn1(1,3)/mag;
        atomid(jatom)=id;
        xnew(jatom) = xnew(jatom-1) + uvx*lc;
        ynew(jatom) = ynew(jatom-1) + uvy*lc;
        znew(jatom) = znew(jatom-1) + uvz*lc;

        while((xnew(jatom)>Lx1 & xnew(jatom)<Lx2) & ...
            (ynew(jatom)>Ly1 & ynew(jatom)<Ly2) & ...
            (znew(jatom)>Lz1 & znew(jatom)<Lz2))

            iflag = iflag+1;

            if (iflag > 100)
                break
            end

            rn=rand(1,3); rn1(1,1)=rn(1,1)-0.5; rn1(1,2)=rn(1,2)-0.5; rn1(1,3)=rn(1,3)-0.5;
            mag=sqrt(rn1(1,1)^2 + rn1(1,2)^2 + rn1(1,3)^2); %magnititude
            uvx=rn1(1,1)/mag;
            uvy=rn1(1,2)/mag;
            uvz=rn1(1,3)/mag;
            atomid(jatom)=id;
            xnew(jatom) = xnew(jatom-1) + uvx*lc;

```

```

    ynew(jatom) = ynew(jatom-1) + uvy*lc;

    znew(jatom) = znew(jatom-1) + uvz*lc;
end
end

%Check whether two atoms' positions are within the tolerance

if (imole==1)
for ipatom=2:jatom
    testid=1;
    iter=1;
    while (testid > 0.1 & iter <= 50 )
        iter=iter+1;
        testid=0;
        for itest=1:(ipatom-1)
            dist= sqrt((xnew(ipatom)-xnew(itest))^2+(ynew(ipatom)- ynew(itest))^2+(znew(ipatom)-
                znew(itest))^2);

            if dist < toler;
                testid=testid+1;
            end
        end
    end

    if (testid > 0.1)
        rn=rand(1,3); rn(1,1)=rn(1,1)-0.5; rn(1,2)=rn(1,2)-0.5; rn(1,3)=rn(1,3)-0.5;

        % Magnitude
        mag=sqrt(rn(1,1)^2 + rn(1,2)^2 + rn(1,3)^2);
        uvx=rn(1,1)/mag;
        uvy=rn(1,2)/mag;
        uvz=rn(1,3)/mag;
        xnew(ipatom) = xnew(ipatom-1) + uvx*lc;
        ynew(ipatom) = ynew(ipatom-1) + uvy*lc;
        znew(ipatom) = znew(ipatom-1) + uvz*lc;
        iflag=0;
        while((xnew(jatom)>Lx1 & xnew(jatom)<Lx2) & ...
            (ynew(jatom)>Ly1 & ynew(jatom)<Ly2) & ...
            (znew(jatom)>Lz1 & znew(jatom)<Lz2))

            iflag=iflag+1;

            if (iflag > 100)
                break
            end
            rn=rand(1,3); rn(1,1)=rn(1,1)-0.5; rn(1,2)=rn(1,2)-0.5; rn(1,3)=rn(1,3)-0.5;
            mag=sqrt(rn(1,1)^2 + rn(1,2)^2 + rn(1,3)^2); %magnitude
            uvx=rn(1,1)/mag;
            uvy=rn(1,2)/mag;
            uvz=rn(1,3)/mag;
            atomid(jatom)=id;
            xnew(ipatom) = xnew(ipatom-1) + uvx*lc;
            ynew(ipatom) = ynew(ipatom-1) + uvy*lc;
            znew(ipatom) = znew(ipatom-1) + uvz*lc;
        end
    end
end
end

```

```

end
if (iter > 49)
    break
end
end
else
for ipatom=(imole-1)*N+1:jatom
    testid=1;
    iter=1;
    while (testid > 0.1 & iter < 50 )
        iter=iter+1;
        testid=0;
        for itest=1:(ipatom-1)
            dist = sqrt((xnew(ipatom)-xnew(itest))^2+(ynew(ipatom)- new(itest))^2+(znew(ipatom)
                -znew(itest))^2);
            if dist < toler;
                testid=testid+1;
            end
        end
    end

    if (testid > 0.1)
        rn=rand(1,3); rn1(1,1)=rn(1,1)-0.5; rn1(1,2)=rn(1,2)-0.5; rn1(1,3)=rn(1,3)-0.5;

        %Magnitude
        mag=sqrt(rn1(1,1)^2 + rn1(1,2)^2 + rn1(1,3)^2);

        uvx=rn1(1,1)/mag;
        uvy=rn1(1,2)/mag;
        uvz=rn1(1,3)/mag;
        xnew(ipatom) = xnew(ipatom-1) + uvx*lc;
        ynew(ipatom) = ynew(ipatom-1) + uvy*lc;
        znew(ipatom) = znew(ipatom-1) + uvz*lc;
        iflag=0;

        while((xnew(jatom)>Lx1 & xnew(jatom)<Lx2) & ...
            (ynew(jatom)>Ly1 & ynew(jatom)<Ly2) & ...
            (znew(jatom)>Lz1 & znew(jatom)<Lz2))

            iflag=iflag+1;

            if (iflag > 100)
                break
            end

            rn=rand(1,3); rn1(1,1)=rn(1,1)-0.5; rn1(1,2)=rn(1,2)-0.5; rn1(1,3)=rn(1,3)-0.5;
            mag=sqrt(rn1(1,1)^2 + rn1(1,2)^2 + rn1(1,3)^2); %magnitude
            uvx=rn1(1,1)/mag;
            uvy=rn1(1,2)/mag;
            uvz=rn1(1,3)/mag;
            atomid(jatom)=id;
            xnew(ipatom) = xnew(ipatom-1) + uvx*lc;
            ynew(ipatom) = ynew(ipatom-1) + uvy*lc;
            znew(ipatom) = znew(ipatom-1) + uvz*lc;
        end
    end
end
end

```

```

end
if (iter > 49)
    break
end
end
end
end
    irstart=jatom-N+1;
    iend=jatom;
    plot3(xnew(istart:iend),ynew(istart:iend),znew(istart:iend))
%     axis([0 Lx 0 Ly 0 Lz])
    xlabel('x-axis'); ylabel('y-axis'); zlabel('z-axis');
    hold on
end

%Plot to see internal cube
j_atom=1; j_atom2=1; j_atom3=1; j_atom4=1; j_atom5=1; j_atom6=1;
mole = 1;
distance = 4.05*2;
internal_natom=0;
for mole = (1:9)
    %.... assign positions of first four atoms
    xmole(j_atom) = Lx1 + 6*2;
    ymole(j_atom) = Ly1 + 6*2;
    zmole(j_atom) = Lz1 + 6*2;

    xmole(j_atom+1) = xmole(j_atom);
    ymole(j_atom+1) = ymole(j_atom);
    zmole(j_atom+1) = zmole(j_atom);

    xmole(j_atom+2) = xmole(j_atom+1);
    ymole(j_atom+2) = ymole(j_atom+1);
    zmole(j_atom+2) = zmole(j_atom+1);

    xmole(j_atom+3) = xmole(j_atom+2);
    ymole(j_atom+3) = ymole(j_atom+2);
    zmole(j_atom+3) = zmole(j_atom+2);

    xmole(j_atom+4) = xmole(j_atom+3);
    ymole(j_atom+4) = ymole(j_atom+3);
    zmole(j_atom+4) = zmole(j_atom+3);

    xmole(j_atom+5) = xmole(j_atom+4);
    ymole(j_atom+5) = ymole(j_atom+4);
    zmole(j_atom+5) = zmole(j_atom+4);

    xmole(j_atom+6) = xmole(j_atom+5);
    ymole(j_atom+6) = ymole(j_atom+5);
    zmole(j_atom+6) = zmole(j_atom+5);

    xmole(j_atom+7) = xmole(j_atom+6);
    ymole(j_atom+7) = ymole(j_atom+6);
    zmole(j_atom+7) = zmole(j_atom+6);

    xmole(j_atom+8) = xmole(j_atom+7);
    ymole(j_atom+8) = ymole(j_atom+7);
    zmole(j_atom+8) = zmole(j_atom+7);

```

```

%      xmole(j_atom+9) = xmole(j_atom+8);
%      ymole(j_atom+9) = ymole(j_atom+8);
%      zmole(j_atom+9) = zmole(j_atom+8);

      plot3(xmole,ymole,zmole, 'k. ');
      hold on
for IM=1:9
  for JM=1:9
    for KM=1:9
      for IJM=1:9
        internal_natom=internal_natom+1;
        xmole(j_atom+9) = xmole(IJM) + distance*(KM-1);
        ymole(j_atom+9) = ymole(IJM) + distance*(JM-1);
        zmole(j_atom+9) = zmole(IJM) + distance*(IM-1);
      end
      plot3 (xmole,ymole,zmole,'k. ')
      hold on
    end
  end
end
end
internal_natom
for iatom=1:NATOM
  xxx=xnew(iatom); yyy=ynew(iatom); zzz=znew(iatom);

  if ( (xxx>Lx11 & xxx<Lx2) & (yyy>Ly11 & yyy<Ly2) & (zzz>Lz11 & zzz<Lz2))
    plot3(xxx,yyy,zzz,'ro');
  else
%    plot3(xxx,yyy,zzz,'o');
  end
end

hold off

fidin=fopen('molecule_grid.txt','w');
for ii=1:NATOM
  fprintf(fidin,'%5.1f%12.5f%12.5f%12.5f%10.1f
    \n',ii,xnew(ii),ynew(ii),znew(ii),atomid(ii));
end
fclose(fidin);

```


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B. MOLECULAR DYNAMICS

```
% filename: mdss.m version 5.5
%
%
% SSFLAG: input of most material data
% SSPARM: chnage of some parameters (RDEL, VMAX, VDEL) only if necessary
% SSATOM: input of atomic or moclecular masses
% atomid < 10: metals using EAM,
% 10 < atomid < 20: Hydrocarbon using Brenner potential,
% atomid > 20: polymer using Lennard-Jones potential
%
%
%
%
clear
clc
global X Y Z X1 Y1 Z1 X2 Y2 Z2 X3 Y3 Z3 X4 Y4 Z4 X5 Y5 Z5 FX FY FZ;
global IN RL LIST NPOINT NGOFR GR LG;
global ALFA0 ALFA1 ALFA3 ALFA4 ALFA5;
global fid1 fid2 fid3 fid4;
global propty
global P11 P12 P13 P22 P23 P33;
global nrin drin nrhoin drhoin;
global frhoin zrin rhoin rhor frho frhoar frhoar1 frhoar2 frhoar3 frhoar4 frhoar5 frhoar6;
global rhorar rhorar1 rhorar2 rhorar3 rhorar4 rhorar5 rhorar6 z2rar z2rar1 z2rar2 z2rar3 z2rar4
z2rar5 z2rar6;
global nmat atomid amass radcut;
global STRSXX STRSXY STRSXZ STRSYY STRSYZ STRSZZ
global dimsz1 dimsz2 dimsz3 dimsz4

dimsz1=500000;
dimsz2=30000;
dimsz3=450000;
dimsz4=510;
X=zeros(dimsz1,1); Y=zeros(dimsz1,1); Z=zeros(dimsz1,1);
X1=zeros(dimsz1,1); Y1=zeros(dimsz1,1); Z1=zeros(dimsz1,1);
X2=zeros(dimsz1,1); Y2=zeros(dimsz1,1); Z2=zeros(dimsz1,1);
X3=zeros(dimsz1,1); Y3=zeros(dimsz1,1); Z3=zeros(dimsz1,1);
X4=zeros(dimsz1,1); Y4=zeros(dimsz1,1); Z4=zeros(dimsz1,1); radcut=zeros(50,1);
X5=zeros(dimsz1,1); Y5=zeros(dimsz1,1); Z5=zeros(dimsz1,1); amass=zeros(50,1);
FX=zeros(dimsz1,1); FY=zeros(dimsz1,1); FZ=zeros(dimsz1,1); atomid=zeros(dimsz1,1);
IN=zeros(7,1); RL=zeros(26,1); propty=zeros(50,10); LG=zeros(10,1);
LIST=zeros(dimsz2,1); NPOINT=zeros(dimsz2,1); NGOFR=zeros(dimsz2,1);
GR=zeros(dimsz2,1);
ALFA0=zeros(1,1); ALFA1=zeros(1,1); ALFA3=zeros(1,1); ALFA4=zeros(1,1);
ALFA5=zeros(1,1);
frhoin=zeros(dimsz4,2); zrin=zeros(dimsz4,2); rhoin=zeros(dimsz4,2); rhor=zeros(dimsz4,2);
frho=zeros(dimsz4,2); frhoar=zeros(dimsz4,2); frhoar1=zeros(dimsz4,2);
frhoar2=zeros(dimsz4,2); rhoar3=zeros(dimsz4,2); frhoar4=zeros(dimsz4,2);
frhoar5=zeros(dimsz4,2); frhoar6=zeros(dimsz4,2);
rhorar=zeros(dimsz4,2); rhorar1=zeros(dimsz4,2); rhorar2=zeros(dimsz4,2);
rhorar3=zeros(dimsz4,2);
rhorar4=zeros(dimsz4,2); rhorar5=zeros(dimsz4,2); rhorar6=zeros(dimsz4,2);
z2rar=zeros(dimsz4,2,2);
z2rar1=zeros(dimsz4,2,2); z2rar2=zeros(dimsz4,2,2); z2rar3=zeros(dimsz4,2,2);
z2rar4=zeros(dimsz4,2,2);
```

```

z2rar5=zeros(dimz4,2,2); z2rar6=zeros(dimz4,2,2);
P11=zeros(1,1); P12=zeros(1,1); P13=zeros(1,1); P22=zeros(1,1); P23=zeros(1,1);
P33=zeros(1,1);
STRSXX=zeros(dimz1,1); STRSXY=zeros(dimz1,1); STRSXZ=zeros(dimz1,1);
STRSYY=zeros(dimz1,1);
STRSYZ=zeros(dimz1,1); STRSZZ=zeros(dimz1,1);

nrin=1; drin=0.0; nrhoin=1; drhoin=0.0;

% IN(1),KSAMPL),(IN(4),NATOM),(IN(6),NSTEP)
% EQUIVALENCE(LG(1),LENER),(LG(2),LSCALE)
% EQUIVALENCE (RL(16),STPSQH)

%... initialization

fid1=fopen('result1.txt','w');
fid2=fopen('result2.txt','w');
fid3=fopen('result3.txt','w');
fid4=fopen('result4.txt','w'); % stress for each atom
[KRDF,KWRITE,MAXSTP,MAXEQB,NDEAD,DENER]=SSFLAG;

SSPARM;
% SSFCC;
SSATOM;
SSPOTN;
SSIVEL;
SSEVAL;
SSX2SC;

KSAMPL=IN(1);
NATOM=IN(4);
STPSQH=RL(16);
LENER=LG(1);
LSCALE=LG(2);

%... equilibration
for NSTEP = 1:MAXEQB
    IN(6)=NSTEP; NSTEP
    SSPDCT;
    SSEVAL;
    SSCORR;
    SSPRTY;
    if (rem(NSTEP,KWRITE)==0)
        SSMNTR(1);
    end
    if (NSTEP < (MAXEQB-NDEAD))
        if (LSCALE < 0 | LENER < 0)
            SSCALE(DENER);
        end
    end
end
end

SSRSET

```

```
%... production
for NSTEP = 1: MAXSTP
    IN(6)=NSTEP; NSTEP
    SSPDCT;
    SSEVAL;
    SSCORR;
    if (rem(NSTEP,KSAMPL)==0)
        SSPRTY;
    end
    if (rem(NSTEP,KWRITE)==0)
        SSMNTR (KSAMPL);
    end
    if (rem(NSTEP,KRDF)==0)
        SSGOFR;
    end
end

fclose(fid1);
fclose(fid2);
fclose(fid3);
```

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C. AUTOCORRELATION FUNCTION

```
clc
clear
nt=21;
fidinat=fopen('stress.txt');
stress=fscanf(fidinat,'%g %g %g %g %g', [7,nt]);
stress=stress';
fclose(fidinat);
LX=141;
LY=141;
LZ=141;
VOL=LX*LY*LZ;

dt=0.01;

h=1/(2*(nt-1));
Sxy=0; Syz=0; Sxz=0;
Sxy=stress(1,3)^2+stress(nt,3)^2;
Sxz=stress(1,4)^2+stress(nt,4)^2;
Syz=stress(1,6)^2+stress(nt,6)^2;

for i = 2:(nt-1);
    Sxy=Sxy+2*stress(i,3)^2;
    Sxz=Sxz+2*stress(i,4)^2;
    Syz=Syz+2*stress(i,6)^2;
end

Sum=(Sxy+Sxz+Syz)*h/(3*VOL)
```

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